

10414

FIG. 1

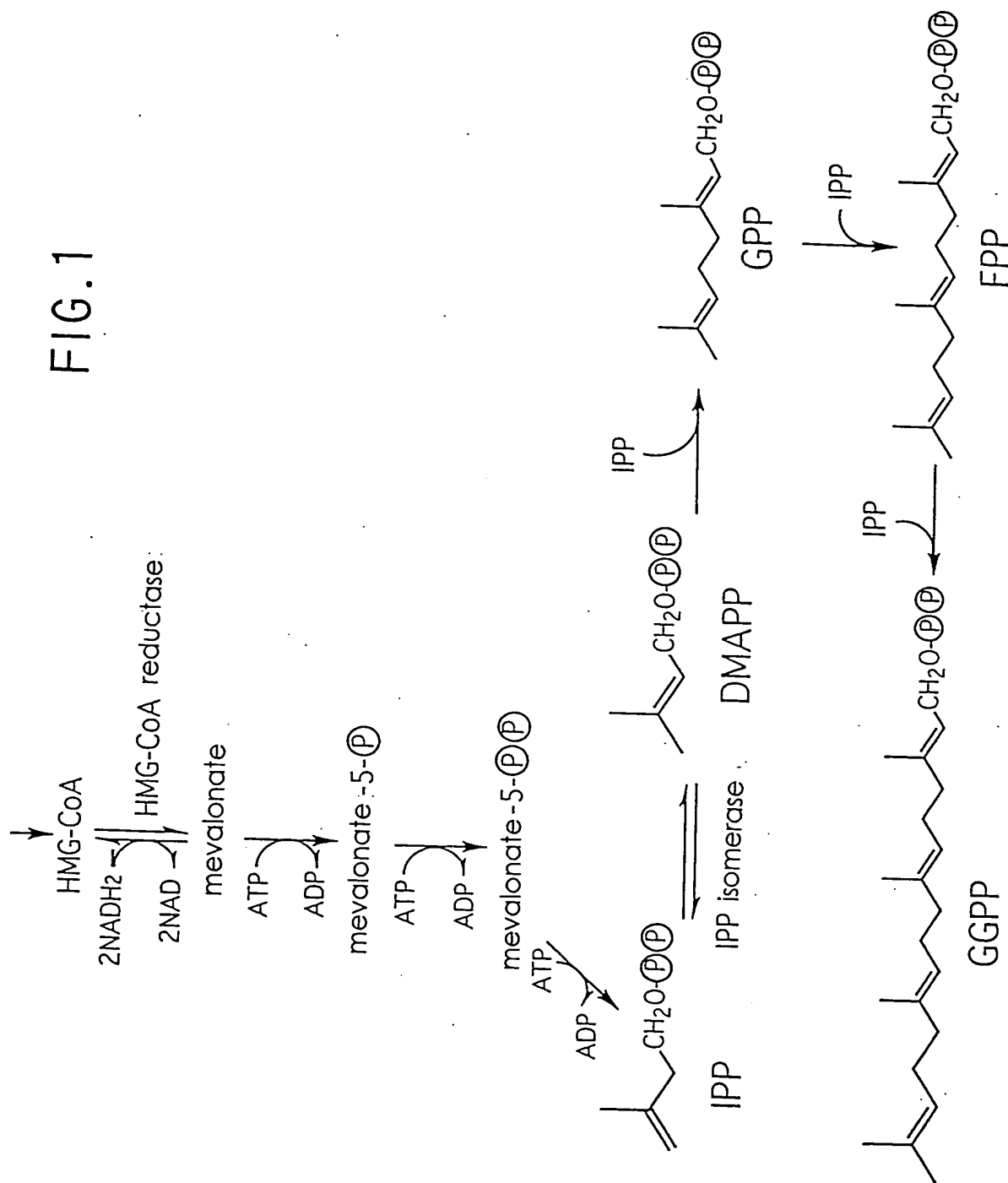


FIG. 2

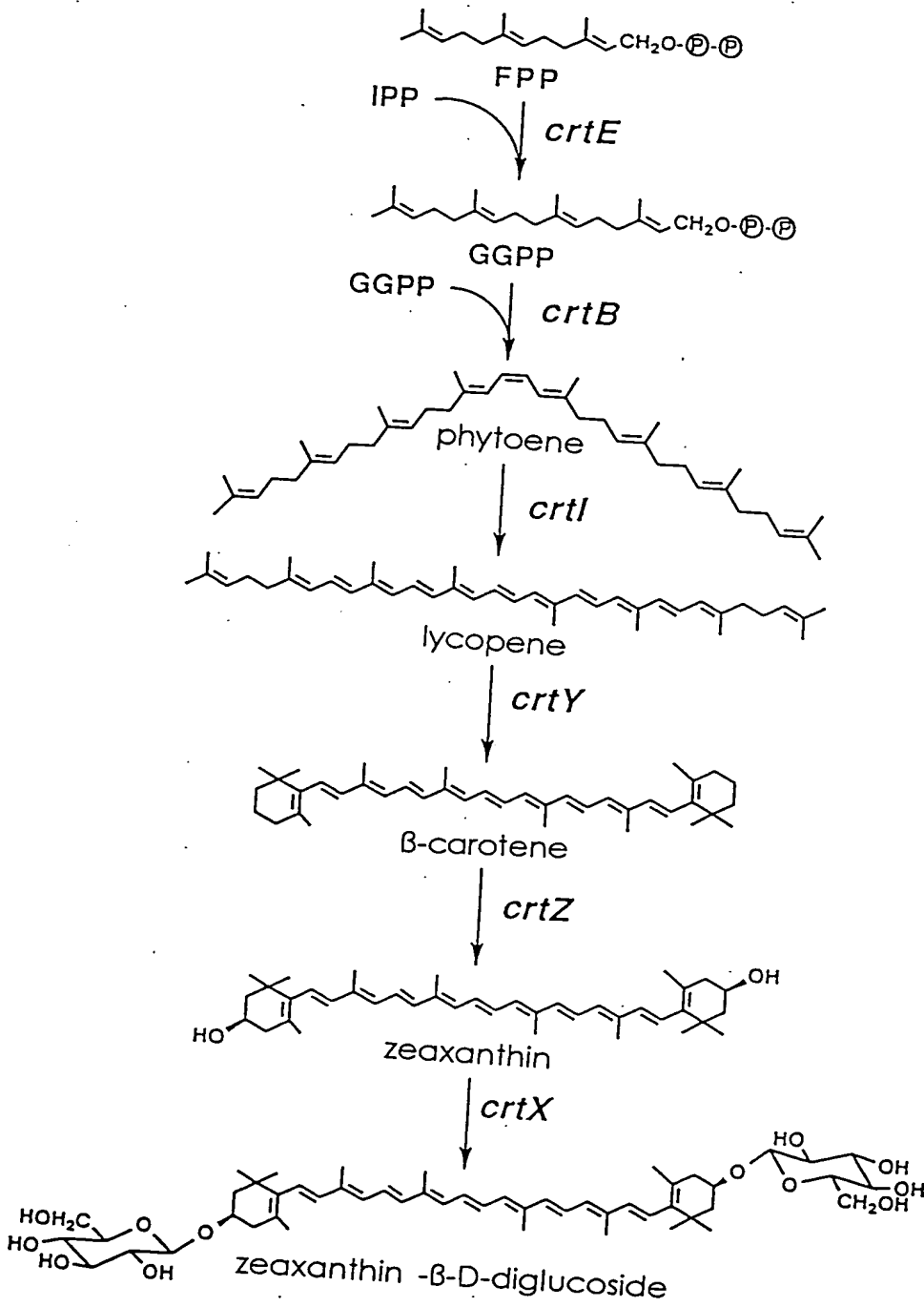


FIG. 3

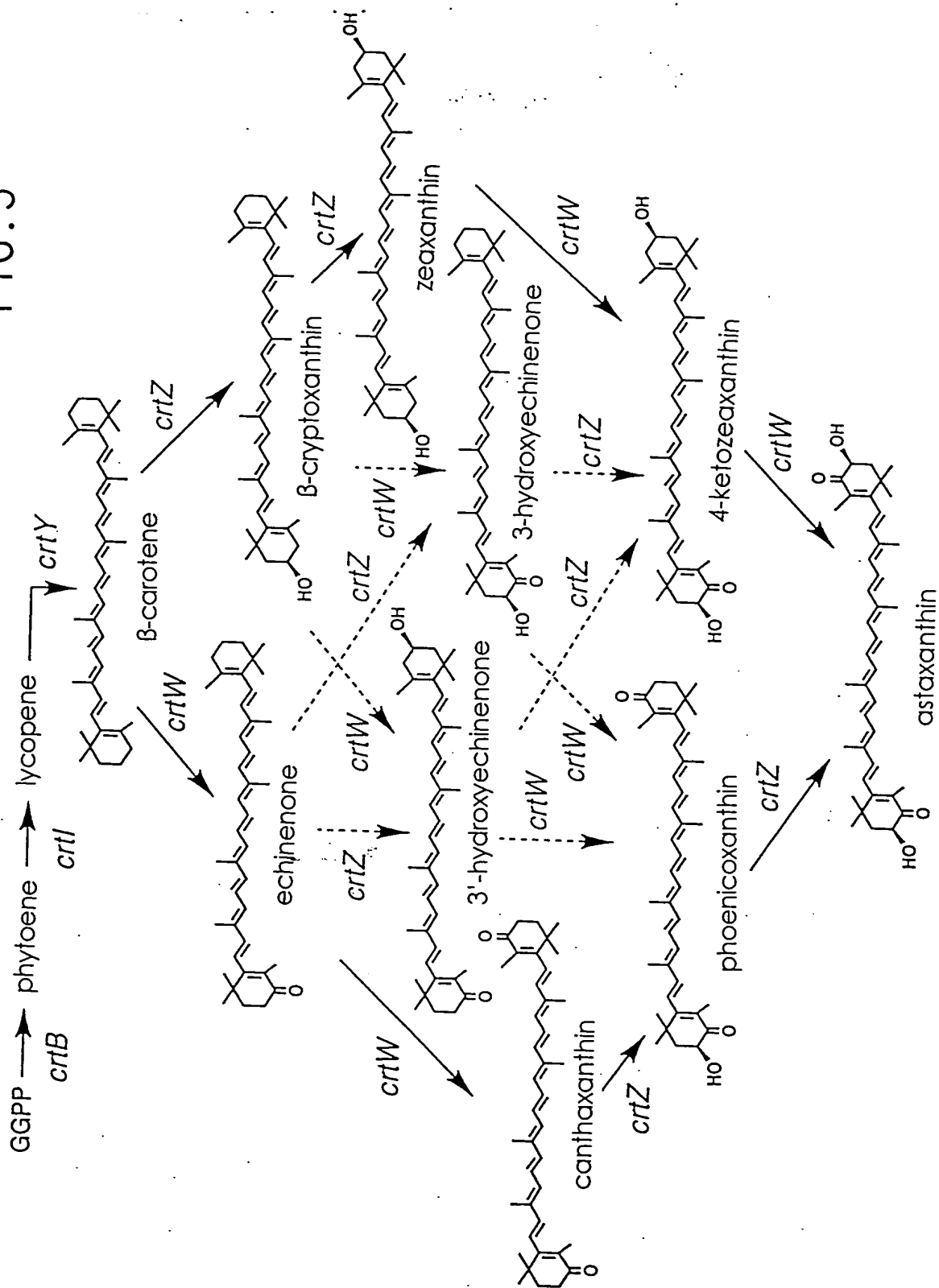


FIG.4

A
 ↓
 9 18 27 36 45 54
 ATG TCC ATG CCC AAC ATT GTT CCC CCC GCC GAG GTC CGA ACC GAA GGA CTC AGT
 Met Ser Met Pro Asn Ile Val Pro Pro Ala Glu Val Arg Thr Glu Gly Leu Ser
 18
 63 72 81 90 99 108
 TTA GAA GAG TAC GAT GAG GAG CAG GTC AGG CTG ATG GAG GAG CGA TGT ATT CTT
 Leu Glu Glu Tyr Asp Glu Glu Gln Val Arg Leu Met Glu Glu Arg Cys Ile Leu
 36
 117 126 135 144 153 162
 GTT AAC CCG GAC GAT GTG GCC TAT GGA GAG GCT TCG AAA AAG ACC TGC CAC TTG
 Val Asn Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser Lys Lys Thr Cys His Leu
 54
 171 180 189 198 207 216
 ATG TCC AAC ATC AAC GCG CCC AAG GAC CTC CTC CAC CGA GCA TTC TCC GTG TTT
 Met Ser Asn Ile Asn Ala Pro Lys Asp Leu Leu His Arg Ala Phe Ser Val Phe
 72
 225 234 243 252 261 270
 CTC TTC CGC CCA TCG GAC GGA GCA CTC CTG CTT CAG CGA AGA GCG GAC GAG AAG
 Leu Phe Arg Pro Ser Asp Gly Ala Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys
 90
 279 288 297 306 315 324
 ATT ACG TTC CCT GGA ATG TGG ACC AAC ACG TGT TGC AGT CAT CCT TTG AGC ATC
 Ile Thr Phe Pro Gly Met Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile
 108
 333 342 351 360 369 378
 AAG GGC GAG GTT GAA GAG GAG AAC CAG ATC GGT GTT CGA CGA GCT GCG TCC CGA
 Lys Gly Glu Val Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg
 126
 387 396 405 414 423 432
 AAG TTG GAG CAC GAG CTT GGC GTG CCT ACA TCG TCG ACT CCG CCC GAC TCG TTC
 Lys Leu Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe
 144
 441 450 459 468 477 486
 ACC TAC CTC ACT AGG ATA CAT TAC CTC GCT CCG AGT GAC GGA CTC TGG GGA GAA
 Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp Gly Glu
 162
 495 504 513 522 531 540
 CAC GAG ATC GAC TAC ATT CTC TTC TCA ACC ACA CCT ACA GAA CAC ACT GGA AAC
 His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu His Thr Gly Asn
 180
 549 558 567 576 585 594
 CCT AAC GAA GTC TCT GAC ACT CGA TAT GTC ACC AAG CCC GAG CTC CAG GCG ATG
 Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys Pro Glu Leu Gln Ala Met
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FIG.5

603	612	621	630	639	648
TTT GAG GAC GAG TCT AAC TCA TTT ACC CCT TGG TTC AAG TTG ATT GCC CGA GAC					
Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro Trp Phe Lys Leu Ile Ala Arg Asp					
					216
657	666	675	684	693	702
TTC CTG TTT GGC TGG TGG GAT CAA CTT CTC GCC AGA CGA AAT GAA AAG GGT GAG					
Phe Leu Phe Gly Trp Trp Asp Gln Leu Leu Ala Arg Arg Asn Glu Lys Gly Glu					
					234
711	720	729	738	747	756
GTC GAT GCC AAA TCG TTG GAG GAT CTC TCG GAC AAC AAA GTC TGG AAG ATG TAG					
Val Asp Ala Lys Ser Leu Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met ***					
					251

B

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FIG.6

C
 ↓
 9 18 27 36 45 54
 ATG CAG CTG CTT GCC GAG GAC CGC ACA GAC CAT ATG AGG GGT GCA AGT ACC TGG
 Met Gln Leu Leu Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp
 63 72 81 90 99 108
 GCA GGC GGG CAG TCG CAG GAT GAG CTG ATG CTG AAG GAC GAG TGC ATC TTG GTG
 Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile Leu Val
 117 126 135 144 153 162
 GAT GCT GAC GAC AAC ATT ACA GGC CAT GTC AGC AAG CTG GAG TGC CAC AAG TTC
 Asp Ala Asp Asp Asn Ile Thr Gly His Val Ser Lys Leu Glu Cys His Lys Phe
 171 180 189 198 207 216
 CTA CCA CAT CAG CCT GCA GGC CTG CTG CAC CGG GCC TTC TCT GTA TTC CTG TTT
 Leu Pro His Gln Pro Ala Gly Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 225 234 243 252 261 270
 GAC GAC CAG GGG CGA CTG CTG CTG CAA CAG CGT GCA CGA TCA AAA ATC ACA TTC
 Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe
 279 288 297 306 315 324
 CCC AGT GTG TGG ACC AAC ACC TGC TGC AGC CAC CCT CTA CAT GGG CAG ACC CCA
 Pro Ser Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro
 333 342 351 360 369 378
 GAT GAG GTG GAC CAA CTA AGC CAG GTG GCC GAC GGC ACA GTA CCT GGC GCA AAG
 Asp Glu Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys
 387 396 405 414 423 432
 GCT GCT GCC ATC CGC AAG TTG GAG CAC GAG CTG GGG ATA CCA GCG CAC CAG CTG
 Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu
 441 450 459 468 477 486
 CCG GCC AGC GCG TTT CGC TTC CTC ACG CGT TTG CAC TAC TGC GCC GCG GAC GTG
 Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val
 495 504 513 522 531 540
 CAG CCG GCT GCG ACA CAA TCA GCA CTC TGG GGC GAG CAC GAA ATG GAC TAC ATC
 Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp Tyr Ile
 549 558 567 576 585 594
 TTA TTC ATC CGG GCC AAC GTC ACC CTT GCG CCC AAC CCT GAC GAG GTG GAC GAA
 Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp Glu Val Asp Glu
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FIG. 7

603	612	621	630	639	648
GTC AGG TAC GTG ACG CAG GAG GAG CTG CGG CAG ATG ATG CAG CCG GAC AAT GGG					
Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met Met Gln Pro Asp Asn Gly					
					216
657	666	675	684	693	702
TTG CAA TGG TCG CCG TGG TTT CGC ATC ATC GCC GCG CGC TTC CTT GAG CGC TGG					
Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp					
					234
711	720	729	738	747	756
TGG GCT GAC CTA GAC GCG GCC CTG AAC ACT GAC AAA CAC GAG GAT TGG GGA ACG					
Trp Ala Asp Leu Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr					
					252
765	774	780			
GTG CAT CAC ATC AAC GAA GCG TGA					
Val His His Ile Asn Glu Ala ***					
		259			
		D			

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FIG.8

E
 ↓
 9 18 27 36 45 54
 ATG ACT GCC GAC AAC AAT AGT ATG CCC CAT GGT GCA GTA TCT AGT TAC GCC AAA
 Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr Ala Lys
 18
 63 72 81 90 99 108
 TTA GTG CAA AAC CAA ACA CCT GAA GAC ATT TTG GAA GAG TTT CCT GAA ATT ATT
 Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe Pro Glu Ile Ile
 36
 117 126 135 144 153 162
 CCA TTA CAA CAA AGA CCT AAT ACC CGA TCT AGT GAG ACG TCA AAT GAC GAA AGC
 Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu Thr Ser Asn Asp Glu Ser
 54
 171 180 189 198 207 216
 GGA GAA ACA TGT TTT TCT GGT CAT GAT GAG GAG CAA ATT AAG TTA ATG AAT GAA
 Gly Glu Thr Cys Phe Ser Gly His Asp Glu Glu Gln Ile Lys Leu Met Asn Glu
 72
 225 234 243 252 261 270
 AAT TGT ATT GTT TTG GAT TGG GAC GAT AAT GCT ATT GGT GCC GGT ACC AAG AAA
 Asn Cys Ile Val Leu Asp Trp Asp Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys
 90
 279 288 297 306 315 324
 GTT TGT CAT TTA ATG GAA AAT ATT GAA AAG GGT TTA CTA CAT CGT GCA TTC TCC
 Val Cys His Leu Met Glu Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser
 108
 333 342 351 360 369 378
 GTC TTT ATT TTC AAT GAA CAA GGT GAA TTA CTT TTA CAA CAA AGA GCC ACT GAA
 Val Phe Ile Phe Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu
 126
 387 396 405 414 423 432
 AAA ATA ACT TTC CCT GAT CTT TGG ACT AAC ACA TGC TGC TCT CAT CCA CTA TGT
 Lys Ile Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
 144
 441 450 459 468 477 486
 ATT GAT GAC GAA TTA GGT TTG AAG GGT AAG CTA GAC GAT AAG ATT AAG GGC GCT
 Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys Gly Ala
 162
 495 504 513 522 531 540
 ATT ACT GCG GCG GTG AGA AAA CTA GAT CAT GAA TTA GGT ATT CCA GAA GAT GAA
 Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile Pro Glu Asp Glu
 180

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FIG.9

549 558 567 576 585 594
 ACT AAG ACA AGG GGT AAG TTT CAC TTT TTA AAC AGA ATC CAT TAC ATG GCA CCA
 Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg Ile His Tyr Met Ala Pro
 198
 603 612 621 630 639 648
 AGC AAT GAA CCA TGG GGT GAA CAT GAA ATT GAT TAC ATC CTA TTT TAT AAG ATC
 Ser Asn Glu Pro Trp Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Tyr Lys Ile
 216
 657 666 675 684 693 702
 AAC GCT AAA GAA AAC TTG ACT GTC AAC CCA AAC GTC AAT GAA GTT AGA GAC TTC
 Asn Ala Lys Glu Asn Leu Thr Val Asn Pro Asn Val Asn Glu Val Arg Asp Phe
 234
 711 720 729 738 747 756
 AAA TGG GTT TCA CCA AAT GAT TTG AAA ACT ATG TTT GCT GAC CCA AGT TAC AAG
 Lys Trp Val Ser Pro Asn Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys
 252
 765 774 783 792 801 810
 TTT ACG CCT TGG TTT AAG ATT ATT TGC GAG AAT TAC TTA TTC AAC TGG TGG GAG
 Phe Thr Pro Trp Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu
 270
 819 828 837 846 855 864
 CAA TTA GAT GAC CTT TCT GAA GTG GAA AAT GAC AGG CAA ATT CAT AGA ATG CTA
 Gln Leu Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu
 288
 867
 TAA

F

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FIG.10

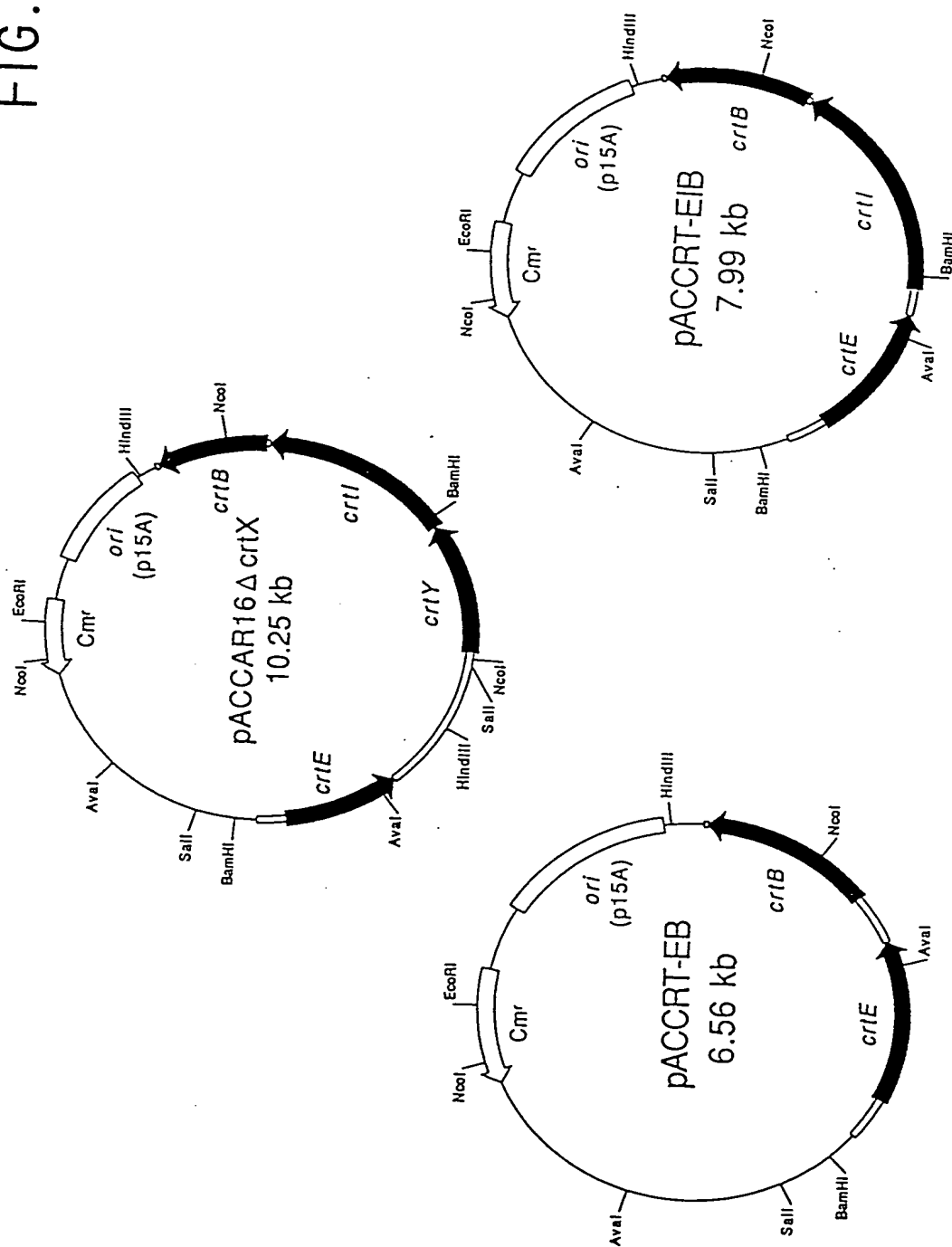
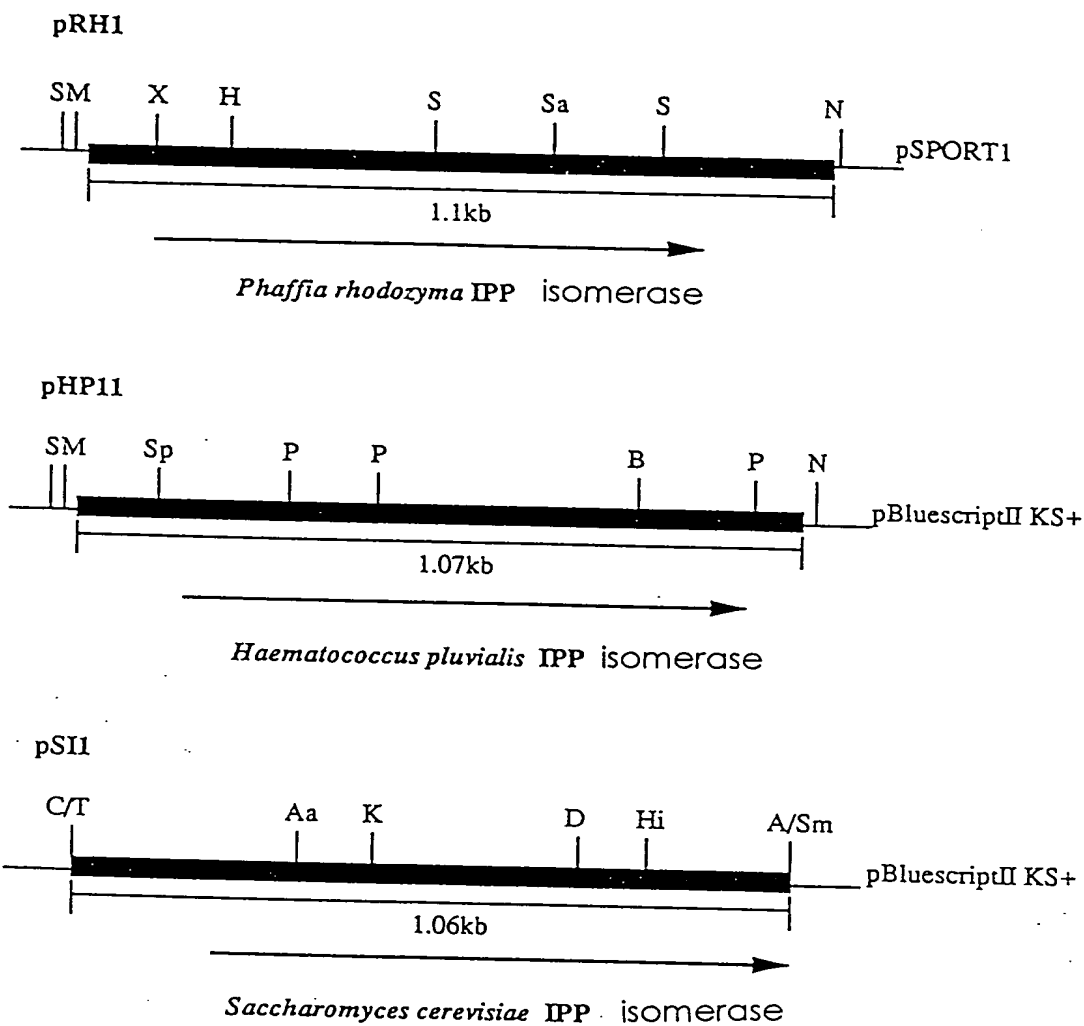


FIG.11



Aa: AatII, A: AccII, B: BssHII, D: DraI, Hi: HincII,
H: HpaI, K: KpnI, M: MluI, N: NotI, P: PstI, Sa: SacI,
S: SalI, Sp: SphI, X: XbaI

FIG. 12

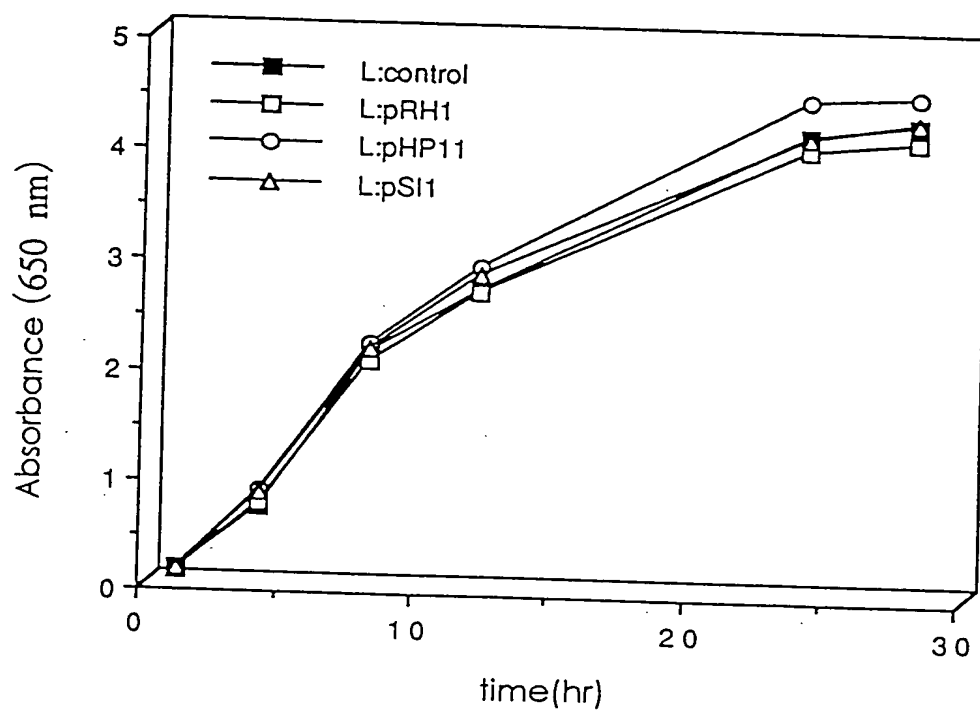


FIG. 13

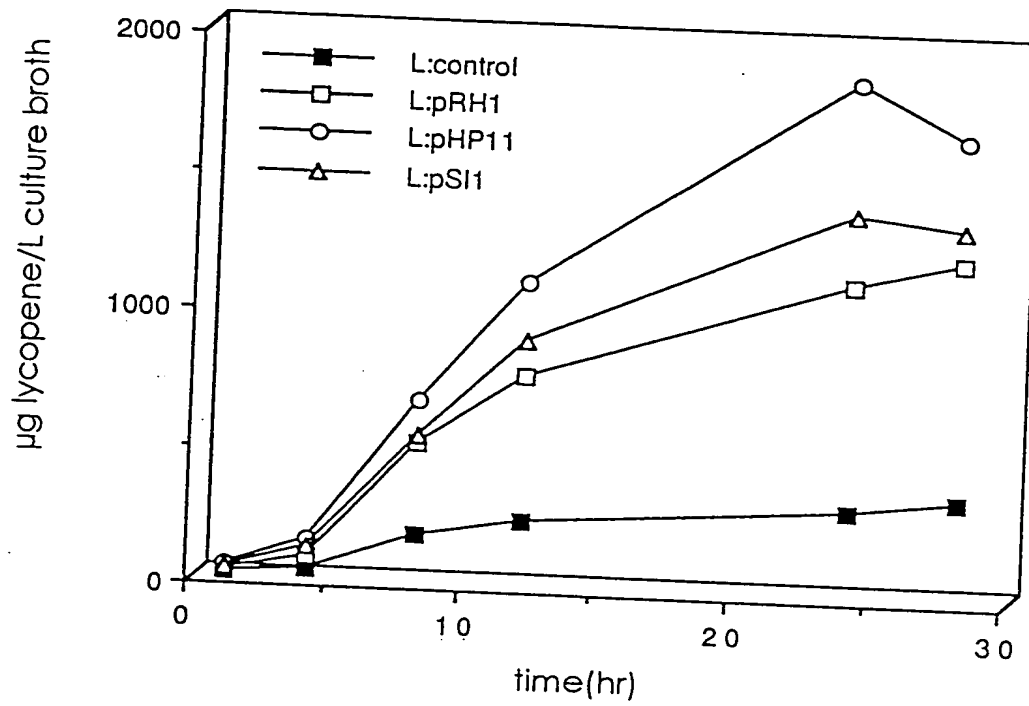


FIG. 14

E.coli	µg carotene/g dry weight	production ratio
L: control	228	1
L: pRH1	825	3.6
L: pHP11	1029	4.5
L: pSI1	859	3.8
β: control	488	1
β: pRH1	709	1.5
P: control	246	1
P: pRH1	413	1.7
P: pHP11	504	2.1